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#10/Seq.
Listing

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/348,815

DATE: 11/06/2000

TIME: 11:22:56

Input Set : A:\126p1d1-sl.txt

Output Set: N:\CRF3\11062000\I348815.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: LI, HAODONG

7 ADAMS, MARK D

9 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR-2

11 (iii) NUMBER OF SEQUENCES: 6

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.

15 (B) STREET: 9410 KEY WEST AVENUE

16 (C) CITY: ROCKVILLE

17 (D) STATE: MD

18 (E) COUNTRY: US

19 (F) ZIP: 20850

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/348,815

C--> 29 (B) FILING DATE: 08-Jul-1999

30 (C) CLASSIFICATION:

32 (viii) ATTORNEY/AGENT INFORMATION:

33 (A) NAME: JONATHAN L. KLEIN

34 (B) REGISTRATION NUMBER: 41,119

35 (C) REFERENCE/DOCKET NUMBER: PF126P1D1

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: 301-309-8504

39 (B) TELEFAX: 301-309-8439

42 (2) INFORMATION FOR SEQ ID NO: 1:

44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1146 base pairs

46 (B) TYPE: nucleic acid

47 (C) STRANDEDNESS: single

48 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

53 (ix) FEATURE:

54 (A) NAME/KEY: CDS

55 (B) LOCATION: 1..1146

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT CTC 48

61 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Val Val Thr Leu Leu

62 1 5 10 15

64 CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC TGC 96

65 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys

66 20 25 30

68 CCC CTG GAG CCG CCC AAG TGC GCG CCG GCA GTC GCG CTG GTC CGG GAC 144

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Input Set : A:\126pldl-sl.txt

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```

69 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
70          35          40          45
72 GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC TGC 192
73 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
74          50          55          60
76 AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC TTC 240
77 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
78 65          70          75          80
80 GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA GAG 288
81 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
82          85          90          95
84 GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGT 336
85 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
86          100          105          110
88 TTC CAG CCC AAC TGT AAA CAT CAG TGC ACA TGT ATT GAT GGC GCC GTG 384
89 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
90          115          120          125
92 GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG GGC 432
93 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
94          130          135          140
96 TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG GAG 480
97 Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
98 145          150          155          160
100 TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG GAC 528
101 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
102          165          170          175
104 GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG TTG 576
105 Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
106          180          185          190
108 ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGC TCA CTG AAG 624
109 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
110          195          200          205
112 CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT TTA 672
113 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
114          210          215          220
116 CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC TCA 720
117 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
118 225          230          235          240
120 AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC CCT 768
121 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
122          245          250          255
124 GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT TGT 816
125 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
126          260          265          270
128 GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC AAG 864
129 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
130          275          280          285
132 ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT TTG 912
133 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu

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Input Set : A:\126pldl-sl.txt

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```

134      290      295      300
136 AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TGC TGC GTG GAC GGC 960
137 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
138 305      310      315      320
140 CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC CGC 1008
141 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
142      325      330      335
144 TGC GAA GAT GCG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG TCC 1056
145 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
146      340      345      350
148 TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT CCC 1104
149 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
150      355      360      365
152 TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT ACG GAC TAA 1146
153 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
154 370      375      380
157 (2) INFORMATION FOR SEQ ID NO: 2:
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 381 amino acids
160 (B) TYPE: amino acid
161 (D) TOPOLOGY: linear
162 (ii) MOLECULE TYPE: protein
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
168 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
169 1 5 10 15
170 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
171 20 25 30
172 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
173 35 40 45
174 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
175 50 55 60
176 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
177 65 70 75 80
178 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
179 85 90 95
180 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
181 100 105 110
182 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
183 115 120 125
184 Gly Cys Ile Pro Leu Cys Pro Gln Gln Leu Ser Leu Pro Asn Leu Gly
185 130 135 140
186 Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
187 145 150 155 160
188 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
189 165 170 175
190 Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
191 180 185 190
192 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
193 195 200 205

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/348,815

DATE: 11/06/2000

TIME: 11:22:56

Input Set : A:\126pld1-s1.txt

Output Set: N:\CRF3\11062000\I348815.raw

```

194 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
195      210      215      220
196 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
197 225      230      235      240
198 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
199      245      250      255
200 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
201      260      265      270
202 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
203      275      280      285
204 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
205      290      295      300
206 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
207 305      310      315      320
208 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
209      325      330      335
210 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
211      340      345      350
212 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
213      355      360      365
214 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
215      370      375      380

```

219 (2) INFORMATION FOR SEQ ID NO: 3:

221 (i) SEQUENCE CHARACTERISTICS:

222 (A) LENGTH: 28 base pairs

223 (B) TYPE: nucleic acid

224 (C) STRANDEDNESS: single

225 (D) TOPOLOGY: linear

227 (ii) MOLECULE TYPE: DNA (genomic)

230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

232 CGCGGGATCC TCGCGGACAC AATGAGCT

28

234 (2) INFORMATION FOR SEQ ID NO: 4:

236 (i) SEQUENCE CHARACTERISTICS:

237 (A) LENGTH: 30 base pairs

238 (B) TYPE: nucleic acid

239 (C) STRANDEDNESS: single

240 (D) TOPOLOGY: linear

242 (ii) MOLECULE TYPE: DNA (genomic)

245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

247 CGCGGGTACC AGGTAGCATT TAGTCCCTAA

30

249 (2) INFORMATION FOR SEQ ID NO: 5:

251 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 27 base pairs

253 (B) TYPE: nucleic acid

254 (C) STRANDEDNESS: single

255 (D) TOPOLOGY: linear

257 (ii) MOLECULE TYPE: DNA (genomic)

260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

262 AAAGGATCCA CAATGAGCTC CCGAATC

27

RAW SEQUENCE LISTING DATE: 11/06/2000
PATENT APPLICATION: US/09/348,815 TIME: 11:22:56

Input Set : A:\126p1d1-sl.txt
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264 (2) INFORMATION FOR SEQ ID NO: 6:
266 (i) SEQUENCE CHARACTERISTICS:
267 (A) LENGTH: 58 base pairs
268 (B) TYPE: nucleic acid
269 (C) STRANDEDNESS: single
270 (D) TOPOLOGY: linear
272 (ii) MOLECULE TYPE: DNA (genomic)
275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
277 CGCTCTAGAT TAAGCGTAGT CTGGGACGTC GTATGGGTAT TGGACAGCC TGTAGAAG 58

VERIFICATION SUMMARY DATE: 11/06/2000
PATENT APPLICATION: US/09/348,815 TIME: 11:22:57

Input Set : A:\126p1d1-s1.txt
Output Set: N:\CRF3\11062000\I348815.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]